| AQSVPYC  | 3 V S Q I K A | PALHSQ        | GYTGS       | NVKVAV   |    |
|----------|---------------|---------------|-------------|----------|----|
| 1        | 10            |               | 20          | 30       |    |
| IDSGIDSS | SHPDLKV       | / A G G A S I | MVPSET      | NPFQDNI  | N  |
|          | 40            | 5             | 0           | 60       |    |
| SHGTHVA  | GTVAA         | LNNSIGV       | LGVAP       | SASLYAV  | 'K |
|          | 70            | 80            |             | 90       |    |
| VLGADGS  | SGQYSW        | IINGIEW       | AIANN       | MDVINMS  | L  |
| 100      |               | 110           |             | 120      |    |
| GGPSGSA  | ALKAAV        | DKAVAS        | SGVVV       | VAAAGNE  | G  |
| 130      |               | 140           | 1           | .50      |    |
| TSGSSST  | VGYPGK        | YPSVIAV       | <b>GAVD</b> | SSNQRASI | F  |
| 160      | 170           | )             | 180         |          |    |
| SSVGPEL  | DVMAPG        | VSIQST        | LPGNK       | YGAYNGT  | S  |
| 190      | 200           |               | 210         | 22       | 0  |
| MASPHVA  | GAAAL         | ILSKHPN       | WTNT        | VRSSLEN  | ΙT |
|          | 230           | 24            | 0           | 250      |    |
| TTKLGDS  | FYYGKG        | LINVQA        | AAQ         |          |    |
| 26       | 0             | 270           | _           |          |    |

GCGCAGTCCGTGCCTTACGGCGTATCACAAATTAAAGCCCCTGCTC TGCACTCTCAAGGCTACACTGGATCAAATGTTAAAGTAGCGGTTAT CGACAGCGTATCGATTCTTCTCATCCTGATTTAAAGGTAGCAGGC GGAGCCAGCATGGTTCCTTCTGAAACAAATCCTTTCCAAGACAAC AACTCTCACGGAACTCACGTTGCCGGCACAGTTGCGGCTCTTAATA ACTCAATCGGTGTATTAGGCGTTGCGCCAAGCGCATCACTTTACGC TGTAAAAGTTCTCGGTGCTGACGGTTCCGGCCAATACAGCTGGATC ATTAACGGAATCGAGTGGCGATCGCAAACAATATGGACGTTATT AACATGAGCCTCGGCGGACCTTCTGGTTCTGCTGCTTTAAAAGCGG CAGTTGATAAAGCCGTTGCATCCGGCGTCGTAGTCGTTGCGGCAGC CGGTAACGAAGGCACTTCCGGCAGCTCAAGCACAGTGGGCTACCC TGGTAAATACCCTTCTGTCATTGCAGTAGGCGCTGTTGACAGCAGC AACCAAAGAGCATCTTTCTCAAGCGTAGGACCTGAGCTTGATGTC ATGGCACCTGGCGTATCTATCCAAAGCACGCTTCCTGGAAACAAA TACGGGGCGTACAACGGTACGTCAATGGCATCTCCGCACGTTGCC GGAGCGGCTGCTTTGATTCTTTCTAAGCACCCGAACTGGACAAACA CTCAAGTCCGCAGCAGTTTAGAAAACACCACTACAAAACTTGGTG ATTCTTCTACTATGGAAAAGGGCTGATCAACGTACAGGCGGCAG **CTCAGTAA** 

FIG. 3

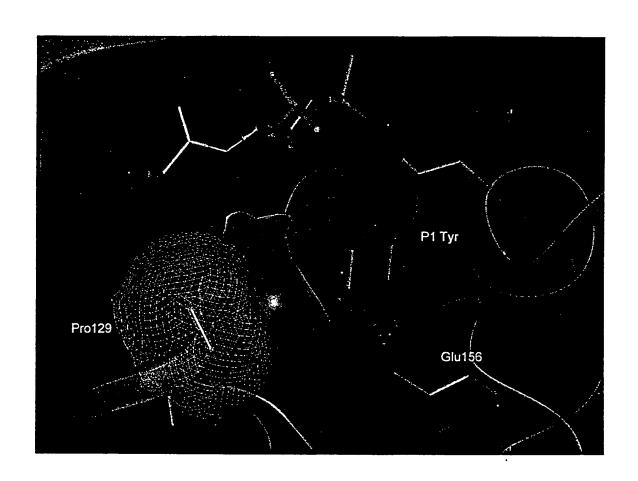


FIG. 4

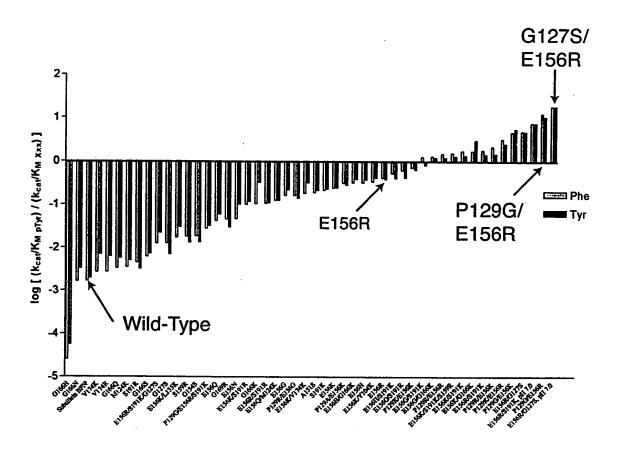
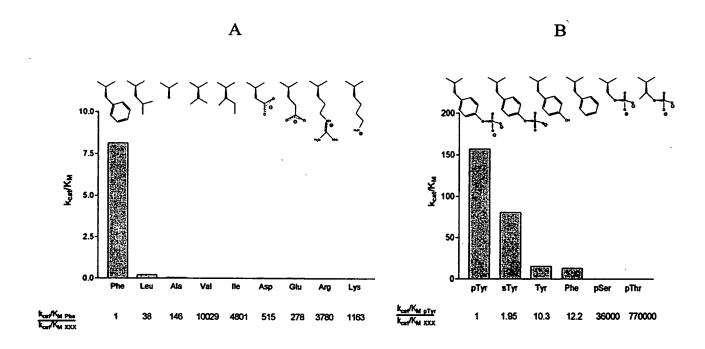


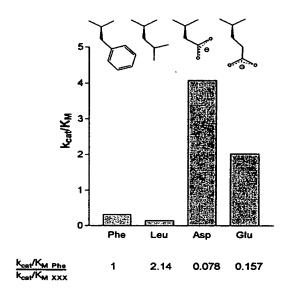
FIG. 5



Suc-Ala-Ala-Pro-Xxx-pNA

Abz-Phe-Arg-Pro-Xxx-Gly-Phe-Y(NO2)-Asp

FIG. 6



MRGKKVWISLLFALALIFTMAFGSTSSAQAAGKSNGEKKYI VGFKQTMSTMSAAKKKDVISEKGGKVQKQFKYVDAASATLN EKAVKELKKDPSVAYVEEDHVAHAYAQSVPYGVSQIKAPALH SQGYTGSNVKVAVIDSGIDSSHPDLKVAGGASMVPSETNPFQD NNSHGTHVAGTVAALNNSIGVLGVAPSASLYAVKVLGADGSG QYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVA SGVVVVAAAGNEGTSGSSSTVGYPGKYPSVIAVGAVDSSNQR ASFSSVGPELDVMAPGVSIQSTLPGNKYGAYNGTSMASPHVA GAAALILSKHPNWTNTQVRSSLENTTTKLGDSFYYGKGLINVQ AAAQ

GTGAGAGGCAAAAAAGTATGGATCAGTTTGCTGTTTGC TTTAGCGTTAATCTTTACGATGGCGTTCGGCAGCACAT CCTCTGCCCAGGCGCAGGGAAATCAAACGGGGAAAAG AAATATATTGTCGGGTTTAAACAGACAATGAGCACGATGA **GCGCCGCTAAGAAGAAGATGTCATTTCTGAAAAAGGCG** GGAAAGTGCAAAAGCAATTCAAATATGTAGACGCAGCTTC **AGCTACATTAAACGAAAAAGCTGTAAAAGAATTGAAAAA** AGACCCGAGCGTCGCTTACGTTGAAGAAGATCACGTAGCA CATGCGTACGCGCAGTCCGTGCCTTACGGCGTATCACAAA TTAAAGCCCCTGCTCTGCACTCTCAAGGCTACACTGGATC AAATGTTAAAGTAGCGGTTATCGACAGCGGTATCGATTCT TCTCATCCTGATTTAAAGGTAGCAGGCGGAGCCAGCATGG TTCCTTCTGAAACAAATCCTTTCCAAGACAACAACTCTCAC GGAACTCACGTTGCCGGCACAGTTGCGGCTCTTAATAACT CAATCGGTGTATTAGGCGTTGCGCCAAGCGCATCACTTTA CGCTGTAAAAGTTCTCGGTGCTGACGGTTCCGGCCAATAC AGCTGGATCATTAACGGAATCGAGTGGGCGATCGCAAACA ATATGGACGTTATTAACATGAGCCTCGGCGGACCTTCTGG TTCTGCTGCTTTAAAAGCGGCAGTTGATAAAGCCGTTGCA TCCGGCGTCGTAGTCGTTGCGGCAGCCGGTAACGAAGGCA CTTCCGGCAGCTCAAGCACAGTGGGCTACCCTGGTAAATA CCCTTCTGTCATTGCAGTAGGCGCTGTTGACAGCAGCAAC CAAAGAGCATCTTTCTCAAGCGTAGGACCTGAGCTTGATG TCATGGCACCTGGCGTATCTATCCAAAGCACGCTTCCTGG AAACAAATACGGGGCGTACAACGGTACGTCAATGGCATCT CCGCACGTTGCCGGAGCGGCTGCTTTGATTCTTTCTAAGCA CCCGAACTGGACAAACACTCAAGTCCGCAGCAGTTTAGAA AACACCACTACAAAACTTGGTGATTCTTTCTACTATGGAA AAGGGCTGATCAACGTACAGGCGGCAGCTCAGTAA